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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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EXAMINER	
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ART UNIT	PAPER NUMBER
1647	10

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Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/056,884	CHANG ET AL.	
	Examiner	Art Unit	
	Christopher Nichols, Ph.D.	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *18 June 2003* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-25* is/are pending in the application.

4a) Of the above claim(s) *5-7,10-15 and 20-25* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-4,8,9 and 16-19* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *24 January 2002* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *5 7* .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

Election/Restrictions

1. Applicant's election of Group I (claims 1-4, 8, 9, and 16-19) drawn to SEQ ID NO: 1, fragments, variants, vectors, and host cell comprising same and method of using said host cells to make a polypeptide in Paper No. 9 (18 June 2003) is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

2. Claims 5-7, 10-15, and 20-25 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected inventions, there being no allowable generic or linking claim. Election was made **without** traverse in Paper No. 9 (18 June 2003).

Specification

3. The disclosure is objected to because of the following informalities: "sequnencer" misspelled (pp. 13 line 18); pp. 27 contains unreadable text, Applicant may supply a replacement copy of pp. 27 of the instant Specification to obviate this objection; "predoimately" is misspelled (pp. 19 line 28); "0.16 um", incorrect symbol (pp. 239 line 22); blank spaces and double parentheses, unclear whether or not text is missing (pp. 273-275). Appropriate correction is required.

4. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code (pp. 223 line 33). Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

5. The use of the trademark RAPAMUNE (among others on pp. 273-275) has been noted in this application. It should be capitalized wherever it appears and be accompanied by the generic terminology.

6. Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner which might adversely affect their validity as trademarks.

Sequence Rules

7. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth below. This application discloses an amino acid sequence on pp. 322. Appropriate correction is required.

Claim Objections

8. Claims **1 and 16** are objected to because of the following informalities: claims 1 and 16 recite non-elected subject matter. Appropriate correction is required.

9. Claims **8 and 9** are objected to because of the following informalities: claims 8 and 9 depend from a non-elected claim. Appropriate correction is required.

10. Claim **4** is objected to because of the following informalities: "sequences" should be replaced by singular, "sequence" as preceding claim is singular "nucleic acid". Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

11. Claims **1-4, 8, 9, and 16-19** are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a well asserted utility or a well established utility.

12. The claims are directed to isolated nucleic acid molecule comprising the amino acid sequence of SEQ ID NO: 1, vectors, and host cells comprising same. The specification asserts that the nucleic acid molecule SEQ ID NO: 1 encodes a polypeptide that is a member of the voltage-gated potassium channel family (therein referred to as K^+ βM2). The specification teaches that voltage-gated potassium channels are a large and diverse family of proteins (pp. 1). The nucleic acid molecule (SEQ ID NO: 1) shares sequence homology to K^+ channel genes, a class known in the art to be large and diverse (pp. 18-19). The art teaches that potassium channels are one of the most diverse groups of ion channels and are classified into three large groups: 2TM-type channels with two transmembrane domains and one P-region, 4TM-type

channels with four transmembrane domains and two P-regions, and 6TM-type channels with six transmembrane domains and one P-region. The diversity of K^+ channels is further increased by alternative splicing and post-translational modification {Nakamura *et al.* "KQT2, a new putative potassium channel family produced by alternative splicing." Receptors Channels **5**(5): 255-271}. The specification discloses no data for any activity of the polypeptide encoded by SEQ ID NO: 1. There are no working examples.

13. There are no well-established utilities for newly discovered biological molecules. However, the specification contains several assertions of utilities. Each will be discussed in turn.

a. *The nucleic acid molecule (SEQ ID NO: 1) encodes a K^+ βM2 (potassium channel) polypeptide:* While the assertion that SEQ ID NO: 1 is a potassium channel is credible based on limited sequence homology, it is neither specific nor substantial because potassium channels are known in the art to be highly diverse. Firstly, the specification's assertion that SEQ ID NO: 1 is a novel K^+ βM2 (potassium channel) polypeptide is not specific. Although the Specification discloses mRNA expression data for SEQ ID NO: 1 in Figure 5, SEQ ID NO: 1 is expressed in a wide range of tissues at varying levels. Therefore it is not clear which potassium channel it is, where it is expressed, what is ligand binding properties are, its inward rectifying properties, or at what levels it is expressed and under what conditions. No specific conclusion can be gained from broad data. The assertion is also not substantial because Barry & Nerbonne (1996) "Myocardial Potassium Channels: Electrophysiological and Molecular Diversity." Annu. Rev. Physiol. **58**: 363-394 teach that potassium channels differ in their time- and voltage-dependent properties and pharmacological sensitivity between species and even

between different areas of the same organ, such as the heart (pp. 363-364). Therefore, the specification's assertion that SEQ ID NO: 1 is a novel K^+ βM2 (potassium channel) polypeptide is not a substantial assertion of utility, since significant further research would be required of the skilled artisan to determine what SEQ ID NO: 1's properties are.

b. *The nucleic acid molecule (SEQ ID NO: 1) encodes a polypeptide that has K^+ βM2 (potassium channel) biological activity:* The specification asserts that SEQ ID NO: 1 encodes a K^+ βM2 (potassium channel) protein based on its structural similarity to prior art of potassium channel polypeptides that have been characterized. This assertion would not have been accepted by one skilled in the art because the art establishes that K^+ channels are both structurally and functionally diverse. For instance, Grupe *et al.* (June 1990) "Cloning and expression of a human voltage-gated potassium channel. A novel member of the RCK potassium channel family." The EMBO Journal 9(6): 1749-1756 teaches the cloning, isolation, and characterization of a novel potassium channel, HBK2 (human brain K^+ channel 2). HBK2 shares 94% sequence homology with the characterized RCK family but does not share its biochemical properties as the two K^+ channels are functionally distinct (Table I and Figure 4). Therefore, no evidence or references are presented to clearly suggest a specific biological activity for SEQ ID NO: 1. In any case, the art clearly shows that sequence similarity to a potassium channel is not predictive of expression patterns or functional similarity (see Table II). Therefore, the specification's assertion that SEQ ID NO: 1 encodes a protein with K^+ channel activity is not a substantial assertion of utility, since significant further research would be required

of the skilled artisan to determine what those activities are. Nor it is specific because it is not known which potassium channel is claimed.

c. *The nucleic acid molecule (SEQ ID NO: 1) can be used to make polypeptides for analysis, characterization, or therapeutic uses:* This asserted utility is not specific or substantial. In recombinantly expressing a polypeptide, the polynucleotide is transfected into a host cell and then the protein is recovered. However, the instant specification does not disclose any known function for the claimed polypeptide or any disease state, toxin, or poison associated with SEQ ID NO: 1. In addition, this utility assertion is not specific as it can be applied to any given polynucleotide. Therefore, it is not clear how the skilled artisan would use a polypeptide manufactured by this method, for analysis, characterization, or therapeutic uses. Since significant further research would be required to determine how to use the identified polynucleotide, the asserted utility is not substantial. And since significant further research would be required to determine the specifics of SEQ ID NO: 1, it is not a specific assertion.

d. *The polypeptide encoded by the nucleic acid molecule (SEQ ID NO: 1) does not have a known ligand:* The specification does not identify any specific ligands for the claimed potassium channel polypeptide encoded by SEQ ID NO: 1 that have been identified. In respect to potassium channels, their expression on different cell types, binding, and response to ligands is highly variable {Catterall (1995) "Structure and Function of voltage-gated ion channels." Annu. Rev. Biochem. **64**: 493-531}. A skilled artisan would have had to experiment significantly to identify the antigen or any allergy or disease or disorder associated with SEQ ID NO: 1. Therefore, the asserted utility is not

substantial. The asserted utility is also not specific, since all receptors can be used to screen for ligands.

e. *The nucleic acid molecule (SEQ ID NO: 1) can be used in drug design:* While credible this asserted utility is also not specific or substantial. In such design paradigms, compounds are screened for their ability to up-regulate or down-regulate expression of the polypeptide or its activity. Compounds that have on or the other activity are then labeled as potential drugs. However, the instant specification does not disclose any specific disease state wherein there is a change in SEQ ID NO: 1 expression levels or forms (i.e., mutations) or activity. In addition, this utility assertion is not specific as it can be applied to any given polypeptide encoded by a nucleic acid or the nucleic acid itself. Therefore, it is not clear how the skilled artisan would use a potential drug identified by this method. This assertion is not specific as it is not known what condition, diseases, or disorders would be the target of the designed drugs nor is it substantial since significant further research would be required to determine how to use the identified potential drugs.

f. *The nucleic acid molecule (SEQ ID NO: 1) is useful as probes or primers:* The specification asserts that the polynucleotides are useful as probes to detect genes encoding SEQ ID NO: 1 or variants thereof, as primers to amplify corresponding gene fragments, to identify potential genetic disorders, or in anti-sense technology to regulate gene expression of SEQ ID NO: 1. This asserted utility is credible, but is neither substantial nor specific. Since there is no substantial utility for the encoded polypeptide, there is also no substantial utility for the nucleic acid probes to identify such. It would take significant further research to determine if the polynucleotide could be used as

probes for particular diseases, since no nexus between a disease state and an alteration in SEQ ID NO: 1 expression levels or form (i.e., mutations) has been disclosed in the specification. Further, since all nucleic acids can be used as probes or primers, this asserted utility is not specific.

g. *The nucleic acid molecule (SEQ ID NO: 1) has therapeutic uses (gene therapy):* This asserted utility is also not substantial. The instant specification does not disclose any known disease state, toxin, or poison associated with SEQ ID NO: 1 or its activity. Therefore, it is not clear how the skilled artisan would use the polynucleotide, for therapeutic uses. Since significant further research would be required to determine how to use the identified polynucleotide, the asserted utility is not substantial. This assertion is also not specific as it is not clear which diseases, conditions, or disorders would be treated via administration of SEQ ID NO: 1.

h. *The nucleic acid molecule (SEQ ID NO: 1) is useful in screening assays (microchip, PCR-based, yeast-based, RLFP):* Again, this asserted utility would only be substantial if the encoded polypeptide has a substantial utility. Otherwise, significant further research would be required of the skilled artisan to use the claimed nucleic acid molecules to use the screening assays, since it is unclear when it would be desirable to use information gained from said assays. This is also not specific as any given nucleic acid molecule can be used in screening assays.

i. *The nucleic acid molecule (SEQ ID NO: 1) can be used to make antisense and/or sense methodology, ribozymes, and peptide nucleic acids (PNA):* Again, this asserted utility would only be substantial if the encoded polypeptide has a substantial utility.

Otherwise, significant further research would be required of the skilled artisan to use the claimed nucleic acid molecules to use said molecules, since it is unclear when it would be desirable to use said molecules. This is also not specific as any given nucleic acid molecule can be used to make antisense, ribozymes, or PNA molecules.

j. *The nucleic acid molecule (SEQ ID NO: 1) can be used to make antigenic peptides:* This utility is also not substantial, because there is no substantial utility for the full length polypeptide. If substantial further research is required to determine how to use the full-length polypeptide, then substantial further research is also required to determine how to use antibodies generated from antigenic fragments. This is also not specific as any given nucleic acid molecule can be used to make antigenic peptides.

k. *The nucleic acid molecule (SEQ ID NO: 1) can be used to make chimeric (fusion) proteins:* This asserted utility is not substantial. The instant specification does not disclose any known disease state, toxin, or poison associated with SEQ ID NO: 1 or its activity. Therefore, it is not clear how the skilled artisan would use a chimeric polypeptide for therapeutic, diagnostic, or research uses. Since significant further research would be required to determine how to use the identified chimeric polypeptide, the asserted utility is not substantial. This is also not specific as any given nucleic acid molecule can be used to make chimeric proteins.

l. *The nucleic acid molecule (SEQ ID NO: 1) can be used to transform host cells:* No phenotype has been disclosed for such transformed host cells. In the absence of such disclosure, the skilled artisan would have to experiment significantly in order to determine how the transformed host cells could be used. Therefore, the asserted utility is

not substantial. This is also not specific as any given nucleic acid molecule can be used to make transformed host cells.

m. *The nucleic acid molecule (SEQ ID NO: 1) can be used in chromosome mapping:* At least nineteen different genes encode known mammalian potassium channels {Kalman *et al.* (6 March 1998) "Genomic Organization, Chromosomal Localization, Tissue Distribution, and Biophysical Characterization of a Novel Mammalian *Shaker*-related Voltage-Gated Potassium Channel, Kv1.7" The Journal of Biological Chemistry **273**(10): 5851-5857}. In order to be useful as a chromosomal probe, the precise chromosomal map position must be disclosed. Substantial further research would be required for the skilled artisan to determine where this particular sequence is mapped in order to use the nucleic acid molecule in the asserted utility as a chromosomal map probe. In addition, no known function has been established for SEQ ID NO: 1. The asserted utility is also not specific, since the entire class of genes can be asserted to be used in this way.

n. *The nucleic acid molecule can be used as molecular weight markers on gels:* This asserted utility is not substantial or specific. For markers, the polynucleotide of interest is digested to yield a reproducible and predicable pattern of fragments or "DNA ladder". However, the instant specification does not disclose any distinct or unique attribute associated with SEQ ID NO: 1 that would motivate on of ordinary skill in the art to use the polynucleotides for such a purpose. In addition, this utility assertion is not specific as it can be applied to any given polynucleotide. Therefore, it is not clear how the skilled artisan would use a set of molecular weight markers or "DNA ladder" manufactured by this method, for analytical uses. Since significant further research would be required to

determine how to use the identified molecular weight markers, the asserted utility is not substantial.

o. *The nucleic acid molecule (SEQ ID NO: 1) can be used to make probes and oligomers:* The specification asserts that the polypeptide (SEQ ID NO: 1) is useful as probes to detect genes encoding SEQ ID NO: 1 or variants thereof, to identify potential genetic disorders, or to regulate gene expression of SEQ ID NO: 1. This asserted utility is credible, but is neither substantial nor specific. Since there is no substantial utility for the polypeptide, there is also no substantial utility for the probes to identify SEQ ID NO: 1 in tissues or biological samples. It would take significant further research to determine if the instantly claimed potassium channel could be used as probes for particular diseases, since no nexus between a disease state and an alteration in SEQ ID NO: 1 expression levels or form (i.e., mutations) has been disclosed in the specification. Also, all polypeptides can be used as "probes" or "oligomers" to detect the genes encoding them, thus the asserted utility is not specific.

p. *The nucleic acid molecule (SEQ ID NO: 1) can be used to make transgenic animals:* No phenotype has been disclosed for such transgenic animals. In the absence of such disclosure, the skilled artisan would have to experiment significantly in order to determine how the transgenic animals could be used. Therefore, the asserted utility is not substantial. This is also not specific as any given nucleic acid molecule can be used to make transgenic animals.

14. Therefore, in the absence of a well-established utility, and the absence of a specific, substantial and credible asserted utility, the claimed invention lacks patentable utility under 35 U.S.C. § 101.

15. If Applicant can submit evidence (in the form of a declaration under 37 CFR 1.132 or post-filing date publications) supporting the specification's assertion that SEQ ID NO: 1 has a specific function similar to a known human potassium channel beta-subunit $K^+\beta M2$, wherein the specific function was predicted by the specification as originally filed, such would be viewed favorably as evidence of patentable utility.

16. Claims **1-4, 8, 9, and 16-19** are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a well asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

17. In addition, regarding derivatives and fragments of SEQ ID NO: 1, the problem of predicting protein structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex. While it is known that many amino acid substitutions are generally possible in any given protein the positions within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of success are limited. Certain positions in the sequence are critical to the protein's structure/function relationship, e.g. such as various sites or regions directly involved in binding, activity and in providing the correct three-dimensional spatial orientation of binding and active sites. These or other regions may also be critical determinants of antigenicity. These

regions can tolerate only relatively conservative substitutions or no substitutions [see Wells (18 September 1990) "Additivity of Mutational Effects in Proteins." Biochemistry **29**(37): 8509-8517; Ngo *et al.* (2 March 1995) "The Protein Folding Problem and Tertiary Structure Prediction, Chapter 14: Computational Complexity Protein Structure Prediction, and the Levinthal Paradox" pp. 492-495]. However, Applicant has provided little or no guidance beyond the mere presentation of sequence data to enable one of ordinary skill in the art to determine, without undue experimentation, the positions in the protein which are tolerant to change (e.g. such as by amino acid substitutions or deletions), and the nature and extent of changes that can be made in these positions. Although the specification outlines art-recognized procedures for producing and screening for active muteins, this is not adequate guidance as to the nature of active derivatives that may be constructed, but is merely an invitation to the artisan to use the current invention as a starting point for further experimentation. Even if an active or binding site were identified in the specification, they may not be sufficient, as the ordinary artisan would immediately recognize that an active or binding site must assume the proper three-dimensional configuration to be active, which conformation is dependent upon surrounding residues; therefore substitution of non-essential residues can often destroy activity. The art recognizes that function cannot be predicted from structure alone [Bork (2000) "Powers and Pitfalls in Sequence Analysis: The 70% Hurdle." Genome Research **10**:398-400; Skolnick and Fetrow (2000) "From gene to protein structure and function: novel applications of computational approaches in the genomic era." Trends in Biotech. **18**(1): 34-39, especially p. 36 at Box 2; Doerks *et al.*, (June 1998) "Protein annotation: detective work for function prediction." Trends in Genetics **14**(6): 248-250; Smith and Zhang (November 1997) "The challenges of genome sequence annotation or

'The devil is in the details'." Nature Biotechnology **15**:1222-1223; Brenner (April 1999) "Errors in genome annotation." Trends in Genetics **15**(4): 132-133; Bork and Bairoch (October 1996) "Go hunting in sequence databases but watch out for the traps." Trends in Genetics **12**(10): 425-427]. Due to the large quantity of experimentation necessary to generate the infinite number of derivatives recited in the claims and possibly screen same for activity, the lack of direction/guidance presented in the specification regarding which structural features are required in order to provide activity, the absence of working examples directed to same, the complex nature of the invention, the state of the prior art which establishes the unpredictability of the effects of mutation on protein structure and function, and the breadth of the claims which fail to recite any structural or functional limitations, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope.

18. Thus the specification of the instant application fails to provide adequate guidance for one of skill in the art to overcome the unpredictability and challenges of applying results from a hypothesized identity and function of a full-length protein to fragments and variants thereof as exemplified in the references herein.

19. Claims **1-4 and 16** are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

20. The claims are drawn to nucleic acids having at least 99.8% sequence identity with a particular disclosed sequence. The claims do not require that the polypeptide possess any

particular conserved structure, or other distinguishing feature, such as a specific biological activity. Thus, the claims are drawn to a genus of nucleic acids that are defined by sequence identity.

21. To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, and any combination thereof. In this case, the only factor present in the claim that is sufficiently disclosed is a partial structure in the form of a recitation of percent identity. The specification does not identify any particular portion of the structure that must be conserved, nor does it provide a disclosure of structure/function correlation. The distinguishing characteristics of the claimed genus are not described. The only adequately described species is a nucleic acid comprising SEQ ID NO: 1. No active variants are disclosed. Accordingly, the specification does not provide adequate written description of the claimed genus.

22. *Vas-Cath Inc. v. Mahurkar*, 19USPQ2d 1111, clearly states "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method

of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

23. One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

24. Therefore, only isolated nucleic acid comprising the sequence set forth in SEQ ID NO: 1, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision.

25. Claim **1** is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

26. Claim 1 is drawn to an "allelic variant of SEQ ID NO: 1", however, no disclosure of the chromosomal location is disclosed. Since the Specification does not disclose the chromosomal location, SEQ ID NO: 1 is novel, hence no guidance can be gained from the prior art, this constitutes an invitation to experiment for the skilled artisan to undertake additional

experimentation to identify the claimed allelic variants. Therefore an undue burden of experimentation is placed on the skilled artisan to practice the invention as claimed.

27. Claim 1 is rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

28. The invention appears to employ novel nucleic acid molecule (i.e., SEQ ID NO: 1). Since the nucleic acid molecule (SEQ ID NO: 1) is essential to the claimed invention they must be obtainable by a repeatable method set forth in the specification or otherwise readily available to the public. If the SEQ ID NO: 1 is not so obtainable or available, the requirements of 35 U.S.C. § 112 may be satisfied by a deposit of the nucleic acid molecules.

29. The specification does not disclose a repeatable process to obtain the nucleic acid molecule and it is not apparent if the nucleic acid molecules are readily available to the public. It is noted that Applicant has deposited the nucleic acid molecule with American Type Culture Collection as ATCC Deposit No. PTA-2966 (pp. 3 and 13 of the specification), but there is no indication in the specification as to public availability.

30. Since the deposit was made under the Budapest Treaty, an affidavit or declaration by Applicant, or a statement by an attorney of record over his or her signature and registration number, stating that the specific nucleic acid molecules have been deposited under the Budapest Treaty and that the nucleic acid molecules will be irrevocably and without restriction or condition released to the public upon the issuance of a patent, would satisfy the deposit requirement made herein. Said affidavit or declaration should include the following:

(a) during the pendency of this application, access to the invention will be afforded to the Commissioner upon request;

(b) all restrictions upon availability to the public will be irrevocably removed upon granting of the patent;

(c) the deposit will be maintained in a public depository for a period of 30 years or 5 years after the last request or for the effective life of the patent, whichever is longer;

(d) a test of the viability of the biological material at the time of deposit will be made (see 37 C.F.R. § 1.807); and

(e) the deposit will be replaced if it should ever become inviable.

31. Applicant's attention is directed to M.P.E.P. §2400 in general, and specifically to §2411.05, as well as to 37 C.F.R. § 1.809(d), wherein it is set forth that "the specification shall contain the accession number for the deposit, the date of the deposit, the name and address of the depository, and a description of the deposited material sufficient to specifically identify it and to permit examination." Finally, Applicant is advised that the address for the ATCC has recently changed, and that the new address should appear in the specification. The new address is:

American Type Culture Collection

10801 University Boulevard

Manassas, VA 20110-2209

32. Claim 1 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The term "stringency" in claim 1 is a relative term which renders the claim indefinite.

The term "stringency" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention. Neither the specification nor the art defines the term unambiguously. Thus the metes and bounds of the claims cannot be determined.

Summary

33. Claims 1-4, 8, 9, and 16-19 are hereby rejected.

34. The following articles, patents, and published patent applications were found by the Examiner during the prior art search and are here made of note:

q. US 5670335 (23 September 1997) Jan *et al.*

r. US 5744324 (28 April 1998) Lester *et al.*

s. US 6309855 B1 (30 October 2001) Duprat *et al.*

t. US 6426197 B1 (30 July 2002) Duckworth *et al.*

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to **Christopher James Nichols, Ph.D.** whose telephone number is 703-305-3955. The examiner can normally be reached on Monday through Friday, 8:00AM to 5:00PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, **Gary Kunz, Ph.D.** can be reached on 703-308-4623. The fax phone numbers for the organization where this application or proceeding is assigned are 703-872-9306 for regular communications and 703-872-9307 for After Final communications. The fax phone numbers for the customer service center is 703-872-9305

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

Elizabeth C. Kemmerer

CJN
September 10, 2003

ELIZABETH KEMMERER
PRIMARY EXAMINER